



x11600.ST25.txt  
SEQUENCE LISTING

<110> Becker, Gerald  
Hale, John  
Heath, William  
Johnstone, Edward  
Little, Sheila  
Tu, Yuan  
Yeh, Wu-Kuang  
Yin, Tinggui

<120> Amyloid Precursor Protein Protease and Related Nucleic Acid Compounds

<130> X-11600

<160> 5

<170> PatentIn version 3.1

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<223> n = any nucleotide A, C, G, or T

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Ser	Val	Thr	Ile	Thr	Pro	Gln	Arg	Ser	Pro	Thr	Gly	Ala	Val	Glu	Val	
235					240					245						
cag	gtc	cct	gag	gac	ccg	gtg	gtg	gcc	cta	gtg	ggc	acc	gat	gcc	acc	819
Gln	Val	Pro	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Gly	Thr	Asp	Ala	Thr	
250					255				260					265		
ctg	cgc	tgc	tcc	tcc	ccc	gag	cct	ggc	ttc	agc	ctg	gca	cag	ctc	867	
Leu	Arg	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu	Ala	Gln	Leu	
270					275					280						
aac	ctc	atc	tgg	cag	ctg	aca	gac	acc	aaa	cag	ctg	gtg	cac	agt	ttc	915
Asn	Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu	Val	His	Ser	Phe	
285					290				295							
acc	gaa	ggc	cgg	gac	cag	ggc	agc	gcc	tat	gcc	aac	cgc	acg	gcc	ctc	963
Thr	Glu	Gly	Arg	Asp	Gln	Gly	Ser	Ala	Tyr	Ala	Asn	Arg	Thr	Ala	Leu	
300					305				310							
ttc	ccg	gac	ctg	ctg	gca	caa	ggc	aat	gca	tcc	ctg	agg	ctg	cag	cgc	1011
Phe	Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala	Ser	Leu	Arg	Leu	Gln	Arg	
315					320				325							
gtg	cgt	gtg	gcg	gac	gag	ggc	agc	ttc	acc	tgc	ttc	gtg	agc	atc	cgg	1059
Val	Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe	Thr	Cys	Phe	Val	Ser	Ile	Arg	
330					335				340				345			
gat	ttc	ggc	agc	gct	gcc	gtc	agc	ctg	cag	gtg	gcc	gct	ccc	tac	tcg	1107
Asp	Phe	Gly	Ser	Ala	Ala	Val	Ser	Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	
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aag	ccc	agc	atg	acc	ctg	gag	ccc	aac	aag	gac	ctg	cgg	cca	ggg	gac	1155
Lys	Pro	Ser	Met	Thr	Leu	Glu	Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asp	
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acg	gtg	acc	atc	acg	tgc	tcc	agc	tac	cgg	ggc	tac	cct	gag	gct	gag	1203
Thr	Val	Thr	Ile	Thr	Cys	Ser	Ser	Tyr	Arg	Gly	Tyr	Pro	Glu	Ala	Glu	
380					385				390							
gtg	tcc	tgg	cag	gat	ggg	cag	ggt	gtg	ccc	ctg	act	ggc	aac	gtg	acc	1251
Val	Phe	Trp	Gln	Asp	Gly	Gln	Gly	Val	Pro	Leu	Thr	Gly	Asn	Val	Thr	
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Thr	Ser	Gln	Met	Ala	Asn	Glu	Gln	Gly	Leu	Phe	Xaa	Xaa	Xaa	Xaa	Xaa	
410					415				420				425			
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Xaa																
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nnn	1395															
Xaa																
445					450				455				455			
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Gln	Pro	Met	Thr	Phe	Pro	Pro	Glu	Ala	Leu	Trp	Val	Thr	Ile	Thr	Gly	
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tct	gtc	tgt	ctc	att	gca	ctg	ctg	gtg	gcc	ctg	gct	ttc	gtg	tgc	tgg	1491
Ser	Val	Cys	Leu	Ile	Ala	Leu	Leu	Val	Ala	Leu	Ala	Phe	Val	Cys	Trp	

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475	480	485	
aga aag atc aaa cag agc tgt gag gag gag aat gca gga gct gag gac Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala Glu Asp 490 495 500 505			1539
cag gat ggg gag gga gaa ggc tcc aag aca gcc ctg cag cct ctg aaa Gln Asp Gly Glu Gly Ser Lys Thr Ala Leu Gln Pro Leu Lys 510 515 520			1587
cac tct gac agc aaa gaa gat gat gga caa gaa ata gcc tga His Ser Asp Ser Lys Glu Asp Asp Gly Gln Glu Ile Ala 525 530			1629
ccatgaggac cagggagctg ctacccctcc ctacagctcc taccctctgg ctgc			1683
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<b>&lt;223&gt;</b> The 'xaa' at location 424 stands for Lys, Asn, Arg, Ser, Thr, Ile			

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Tyr, Trp, Cys, or Phe.

<220>  
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<223> The 'Xaa' at location 425 stands for Lys, Asn, Arg, Ser, Thr, Ile  
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Tyr, Trp, Cys, or Phe.  
  
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<220>

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<220>

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<223> The 'xaa' at location 433 stands for Lys, Asn, Arg, Ser, Thr, Ile , Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>

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<220>

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<223> The 'xaa' at location 435 stands for Lys, Asn, Arg, Ser, Thr, Ile , Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>

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<223> The 'xaa' at location 436 stands for Lys, Asn, Arg, Ser, Thr, Ile , Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

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x11600.ST25.txt

<223> The 'xaa' at location 437 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

<220>

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<223> The 'xaa' at location 438 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

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<223> The 'xaa' at location 440 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

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<223> The 'xaa' at location 443 stands for Lys, Asn, Arg, Ser, Thr, Ile, Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop codon, Tyr, Trp, Cys, or Phe.

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<223> n = any nucleotide A, C, G, or T

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Ala Leu Gly Ala Leu Trp Phe Cys Leu Thr Gly Ala Leu Glu Val Gln  
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Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu  
35 40 45

Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn

50

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55                   60

Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala  
65               70                      75                      80

Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe  
85               90                      95

Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val  
100              105                      110

Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp  
115              120                      125

Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys  
130              135                      140

Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr  
145              150                      155                      160

Val Thr Ile Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val  
165              170                      175

Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr  
180              185                      190

Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Ile Leu  
195              200                      205

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn  
210              215                      220

Pro Val Leu Gln Gln Asp Ala His Ser Ser Val Thr Ile Thr Pro Gln  
225              230                      235                      240

Arg Ser Pro Thr Gly Ala Val Glu Val Gln Val Pro Glu Asp Pro Val  
245              250                      255

Val Ala Leu Val Gly Thr Asp Ala Thr Leu Arg Cys Ser Phe Ser Pro  
260              265                      270

Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr  
275              280                      285

Asp Thr Lys Gln Leu Val His Ser Phe Thr Glu Gly Arg Asp Gln Gly  
290              295                      300

Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln

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Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly			
325	330	335	
Ser Phe Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val			
340	345	350	
Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu			
355	360	365	
Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys Ser			
370	375	380	
Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln			
385	390	395	400
Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met Ala Asn Glu			
405	410	415	
Gln Gly Leu Phe Xaa			
420	425	430	
Xaa Asp			
435	440	445	
Ala His Gly Ser Val Thr Ile Thr Gly Gln Pro Met Thr Phe Pro Pro			
450	455	460	
Glu Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu			
465	470	475	480
Leu Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys			
485	490	495	
Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly			
500	505	510	
Ser Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp			
515	520	525	
Asp Gly Gln Glu Ile Ala			
530			

<210> 3

<211> 1683

<212> DNA

x11600.ST25.txt

<213> Homo sapiens

<220>

<221> CDS

<222> (25)..(1629)

<223>

<220>

<221> misc\_feature

<222> (25)..(1629)

<223>

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x11600.ST25.txt																
140	145	150														
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Asp	Leu	Arg	Pro	Gly	Asp	Thr	Val	Thr	Ile	Thr	Cys	Ser	Ser	Tyr	Gln	
155						160				165						
ggc	tac	cct	gag	gct	gag	gtg	ttc	tgg	cag	gat	ggg	cag	ggt	gtg	ccc	579
Gly	Tyr	Pro	Glu	Ala	Glu	Val	Phe	Trp	Gln	Asp	Gly	Gln	Gly	Val	Pro	
170					175				180					185		
ctg	act	ggc	aac	gtg	acc	acg	tcg	cag	atg	gcc	aac	gag	cag	ggc	ttg	627
Leu	Thr	Gly	Asn	Val	Thr	Thr	Ser	Gln	Met	Ala	Asn	Glu	Gln	Gly	Leu	
190						195								200		
ttt	gat	gtg	cac	agc	atc	ctg	cgg	gtg	gtg	ctg	ggt	gca	aat	ggc	acc	675
Phe	Asp	Val	His	Ser	Ile	Leu	Arg	Val	Val	Leu	Gly	Ala	Asn	Gly	Thr	
205						210							215			
tac	agc	tgc	ctg	gtg	cgc	aac	ccc	gtg	ctg	cag	cag	gat	gcg	cac	agc	723
Tyr	Ser	Cys	Leu	Val	Arg	Asn	Pro	Val	Leu	Gln	Gln	Asp	Ala	His	Ser	
220						225						230				
tct	gtc	acc	atc	aca	ccc	cag	aga	agc	ccc	aca	gga	gcc	gtg	gag	gtc	771
Ser	Val	Thr	Ile	Thr	Pro	Gln	Arg	Ser	Pro	Thr	Gly	Ala	Val	Glu	Val	
235						240					245					
cag	gtc	cct	gag	gac	ccg	gtg	gtg	gcc	cta	gtg	ggc	acc	gat	gcc	acc	819
Gln	Val	Pro	Glu	Asp	Pro	Val	Val	Ala	Leu	Val	Gly	Thr	Asp	Ala	Thr	
250					255					260				265		
ctg	cgc	tgc	tcc	ttc	tcc	ccc	gag	cct	ggc	ttc	agc	ctg	gca	cag	ctc	867
Leu	Arg	Cys	Ser	Phe	Ser	Pro	Glu	Pro	Gly	Phe	Ser	Leu	Ala	Gln	Leu	
270						275							280			
aac	ctc	atc	tgg	cag	ctg	aca	gac	acc	aaa	cag	ctg	gtg	cac	agt	ttc	915
Asn	Leu	Ile	Trp	Gln	Leu	Thr	Asp	Thr	Lys	Gln	Leu	Val	His	Ser	Phe	
285						290						295				
acc	gaa	ggc	cgg	gac	cag	ggc	agc	gcc	tat	gcc	aac	cgc	acg	gcc	ctc	963
Thr	Glu	Gly	Arg	Asp	Gln	Gly	Ser	Ala	Tyr	Ala	Asn	Arg	Thr	Ala	Leu	
300						305						310				
ttc	ccg	gac	ctg	ctg	gca	caa	ggc	aat	gca	tcc	ctg	agg	ctg	cag	cgc	1011
Phe	Pro	Asp	Leu	Leu	Ala	Gln	Gly	Asn	Ala	Ser	Leu	Arg	Leu	Gln	Arg	
315						320					325					
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Val	Arg	Val	Ala	Asp	Glu	Gly	Ser	Phe	Thr	Cys	Phe	Val	Ser	Ile	Arg	
330					335					340				345		
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Asp	Phe	Gly	Ser	Ala	Ala	Val	Ser	Leu	Gln	Val	Ala	Ala	Pro	Tyr	Ser	
350						355							360			
aag	ccc	agc	atg	acc	ctg	gag	ccc	aac	aag	gac	ctg	cgg	cca	ggg	gac	1155
Lys	Pro	Ser	Met	Thr	Leu	Glu	Pro	Asn	Lys	Asp	Leu	Arg	Pro	Gly	Asp	
365						370						375				
acg	gtg	acc	atc	acg	tgc	tcc	agc	tac	cgg	ggc	tac	cct	gag	gct	gag	1203
Thr	Val	Thr	Ile	Thr	Cys	Ser	Ser	Tyr	Arg	Gly	Tyr	Pro	Glu	Ala	Glu	
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Val	Phe	Trp	Gln	Asp	Gly	Gln	Gly	Val	Pro	Leu	Thr	Gly	Asn	Val	Thr	

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395	400	405	
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aac ccc gtg ctg cag cag gat gcg cac ggc tct gtc acc atc aca ggg Asn Pro Val Leu Gln Gln Asp Ala His Gly Ser Val Thr Ile Thr Gly 445 450 455			1395
cag cct atg aca ttc ccc cca gag gcc ctg tgg gtg acc gtg ggg ctg Gln Pro Met Thr Phe Pro Pro Glu Ala Leu Trp Val Thr Val Gly Leu 460 465 470			1443
tct gtc tgt ctc att gca ctg ctg gtg gcc ctg gct ttc gtg tgc tgg Ser Val Cys Leu Ile Ala Leu Leu Val Ala Leu Ala Phe Val Cys Trp 475 480 485			1491
aga aag atc aaa cag agc tgt gag gag gag aat gca gga gct gag gac Arg Lys Ile Lys Gln Ser Cys Glu Glu Glu Asn Ala Gly Ala Glu Asp 490 495 500 505			1539
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Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp Ala Thr Leu  
35 40 45

Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn  
50 55 60

Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu Val His Ser Phe Ala  
65 70 75 80

Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe  
85 90 95

Pro Asp Leu Leu Ala Gln Gly Asn Ala Ser Leu Arg Leu Gln Arg Val  
100 105 110

Arg Val Ala Asp Glu Gly Ser Phe Thr Cys Phe Val Ser Ile Arg Asp  
115 120 125

Phe Gly Ser Ala Ala Val Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys  
130 135 140

Pro Ser Met Thr Leu Glu Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr  
145 150 155 160

Val Thr Ile Thr Cys Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Glu Val  
165 170 175

Phe Trp Gln Asp Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr  
180 185 190

Ser Gln Met Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Ile Leu  
195 200 205

Arg Val Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn  
210 215 220

Pro Val Leu Gln Gln Asp Ala His Ser Ser Val Thr Ile Thr Pro Gln  
225 230 235 240

Arg Ser Pro Thr Gly Ala Val Glu Val Gln Val Pro Glu Asp Pro Val  
245 250 255

Val Ala Leu Val Gly Thr Asp Ala Thr Leu Arg Cys Ser Phe Ser Pro  
260 265 270

Glu Pro Gly Phe Ser Leu Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr  
275 280 285

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Asp Thr Lys Gln Leu Val His Ser Phe Thr Glu Gly Arg Asp Gln Gly  
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Ser Ala Tyr Ala Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln  
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Gly Asn Ala Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly  
325 330 335

Ser Phe Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val  
340 345 350

Ser Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu  
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Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys Ser  
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Ser Tyr Arg Gly Tyr Pro Glu Ala Glu Val Phe Trp Gln Asp Gly Gln  
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Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met Ala Asn Glu  
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Gln Gly Leu Phe Asp Val His Ser Val Leu Arg Val Val Leu Gly Ala  
420 425 430

Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro Val Leu Gln Gln Asp  
435 440 445

Ala His Gly Ser Val Thr Ile Thr Gly Gln Pro Met Thr Phe Pro Pro  
450 455 460 465

Glu Ala Leu Trp Val Thr Val Gly Leu Ser Val Cys Leu Ile Ala Leu  
470 475 480

Leu Val Ala Leu Ala Phe Val Cys Trp Arg Lys Ile Lys Gln Ser Cys  
485 490 495

Glu Glu Glu Asn Ala Gly Ala Glu Asp Gln Asp Gly Glu Gly Glu Gly  
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Ser Lys Thr Ala Leu Gln Pro Leu Lys His Ser Asp Ser Lys Glu Asp  
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Asp Gly Gln Glu Ile Ala  
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x11600.ST25.txt  
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gc 1682